Amendments to the Specification:

Please insert the following Title at page 1, line 1 of the specification:

-- ~~**New transcription**~~ **Transcription factor of MHC Class II genes, substances capable of inhibiting this ~~new~~ transcription factor and medical uses of these substances** --

Please replace the Abstract at page 94 of the specification with the following paragraph:

--The present invention relates to a ~~novel~~ transcription factor of MHC class II genes and its derivatives, inhibitors down-regulating the expression of MHC class II molecules, process to identify these inhibitors and medical uses of these inhibitors.--

Please replace the paragraph at page 54, line 32 through page 55, line 25 with the following paragraph:

--RFXANK was sequenced by capillary liquid chromatography tandem mass spectrometry (LC-MS/MS). The protein excised from the gel was digested with trypsin (Promega, Madison, WI) and extracted as described previously[25]. Prior to LC-MS/MS, the peptides were vacuum dried and resuspended in H2O. Peptides were loaded onto a 75 mm RP-HPLC column, packed with a 200 Å pore, 5 mm particles of Magic C18 packing material (Michrom Bioresources, Auburn, CA) at 1000 psi using a pressure bomb[47]. Subsequent elution was performed at 250 n>/min after fractionation through a splitting Tee (Valco Instruments, Houston, TX) of a linear gradient that was developed for 30 min at 50 mL/min from buffer A (2 % CH3CN, 98 % H2O, 0.4 % CH3COOH, 0.005 % C4HF7O2) to buffer B (80 % CH3CN, 20 % H2O, 0.4 % CH3COOH, 0.005 % C4HF7O2) on a Michrom Ultrafast Microprotein analyzer (Michrom Bioresources, Auburn, CA). Tandem mass spectroscopy was conducted on a Finnigan MAT TSQ 7000 (San Jose, CA) equipped with an in house built microspray device for peptide ionization. The instrument was run in automated mode, where parent masses were automatically selected for fragmentation[48]. Collision induced dissociation (CID) spectra were correlated with database entries using the SEQUEST programme[49] and verified by manual interpretation. Databases used for the CID correlation were the dbOWL ~~http://www.biochem.ucl.ac.uk/bsm/dbbrowser/OWL/OWL.html And~~ and the dbEST

~~(http://www.ncbi.nlm.nih.gov/dbEST/index.html)~~--

Please replace the paragraph at page 56, line13 through page 57, line 22 with the following paragraph:

--The resulting sequence was confirmed by comparison with the genomic sequence and by RT-PCR amplification and sequencing of RFXANK cDNA clones from control B cell lines (Raji and QBL). The following primers were used to amplify RFXANK cDNAs by PCR: 5'p33 (5'-CCGTACGCGTCTAGACCATGGAGCTTACCCAGCCTGCAGA-3') (SEQ ID NO: 1), which overlaps the translation initiation codon, and 3'p33 (5'-TTCGAATTCTCGAGTGTCTGAGTCCCCGGCA-3') (SEQ ID NO: 2), which is complementary to the 3' untranslated region of RFXANK mRNA. Homology to RFXANK mRNA is underlined. The primers contain restriction sites at their 5' ends to facilitate cloning. RFXANK cDNAs were cloned into the expression plasmid EBO-76PL (ref. [8]) and pBluescript KS (Stratagene). 12 RFXANK cDNA clones were sequenced on both strands. The nucleotide and amino acid sequences of human RFXANK were test for homology to sequences in EMBL, GenBank, SwissProt, and dbEST. Sequence analysis was performed with PC/gene (Intelligenetics), BLAST programs available through the NCBI server ~~(http://www.ncbi.nlm.nih.gov)~~, and a variety of proteomics tools <u>from ExPASy</u> ~~(http://www.expasy.ch/www/tools.html)~~. For multiple protein sequence alignments, CLUSTALW ~~(http://www2.ebi.ac.uk/clustalw)~~ was used. ESTs were assembled into contigs with the TIGR Assembler ~~(http://www.tigr.org)~~. The search for homology to human RFXANK identified EST clones corresponding to mouse (AA435121, AA616119, AA259432, AA146531) and rat (AA851701) orthologs, and to a highly homologous gene present in both man (AA496038, AA442702, AA205305, N25678, N70046, AA418029, AA633452, H39858, R86213, AA418089, N64316, R63682, N55216) and mouse (AA245178, Z31339, AA118335). The sequences of mouse Rfxank and of the human and mouse homologues were determined by organizing the corresponding ESTs into contigs. The mouse Rfxank sequence was confirmed by amplifying the cDNA by RT-PCR from C57BL6 mouse spleen RNA using the following primers:

m5'p33 (5'- CCGTACGCGTCTAGACCATGGAGCCCACTGAGGTTGC – 3') (SEQ ID NO:

3), which overlaps the translation initiation codon, and m3'p33 (5' – TTCGAATTCTCGAGTGCCTGGGTTCCAGCAGG – 3') (SEQ ID NO: 4), which is complementary to the 3' untranslated region of Rfxank mRNA. Homology to mouse Rfxank mRNA is underlined. The primers included 5' extensions with restriction sites that were used to clone the mouse Rfxank cDNA directly into the EBO-76PL expression vector[8]. 14 clones were sequenced on both strands.--

Please replace the paragraph at page 67, lines 8-14 with the following paragraph:

--Wild type and mutated DRA promoter fragments were constructed by PCR on a DRsyn template. The W box sequence GGACCCTTTGCAAG (SEQ ID NO: 21) was mutated to TACATAGCGTACGT (SEQ ID NO: 22). The X2 box sequence TGCGTCA (SEQ ID NO: 23) was mutated to GACAAGT (SEQ ID NO: 24). The mutated X and Y templates were described previously. The ~~Oct~~ ΔOct template (-150 to –56) was obtained by the digestion of the wild type DRsyn fragment with BglII.--

Please replace, at the end of the specification, the Sequence Listing submitted February 13, 2002 with the submitted Substitute Sequence Listing, pages 1-11.